

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 21, 2006, 14:39:05 ; Search time 37.0181 Seconds
(without alignments)
938.721 Million cell updates/sec

Title: US-10-539-834-2

Perfect score: 2135

Sequence: 1 MRCPKCLLSALLTLGLK.....LGQASIRLWKLQDPRIQC 397

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents, AA:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pap:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pap:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pap:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/8_COMB.pap:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/9_COMB.pap:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pap:*
- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2131	99.8	397	2	US-09-459-133-2
2	1595	74.7	389	2	US-09-459-133-13
3	558	26.1	397	3	US-10-019-735-1
4	481	22.5	378	3	US-10-019-735-4
5	467	21.9	378	2	US-09-482-180A-2
6	464.5	21.8	372	3	US-10-019-735-3
7	459.5	21.5	372	3	US-10-019-735-2
8	379.5	17.8	378	2	US-10-104-047-2503
9	344.5	16.1	422	2	US-09-831-630-10
10	337	15.8	326	1	US-09-055-097-6
11	337	15.8	326	2	US-09-373-902-6
12	337	15.8	326	2	US-09-831-630-11
13	322.5	15.1	378	1	US-09-055-097-1
14	322.5	15.1	378	2	US-09-373-902-1
15	320.5	15.0	393	2	US-09-949-016-11567
16	320.5	15.0	378	2	US-09-831-630-13
17	314	14.7	310	2	US-09-831-630-9
18	260	12.2	331	2	US-09-831-630-12
19	260	12.2	331	2	US-09-991-181-209
20	260	12.2	331	2	US-09-990-444-209
21	260	12.2	331	2	US-09-997-333-209
22	260	12.2	331	2	US-09-992-598-209
23	260	12.2	331	2	US-09-988-735-209
24	260	12.2	331	3	US-09-989-726-209
25	260	12.2	331	3	US-09-997-514-209
26	260	12.2	331	3	US-09-989-728-209

27	260	12.2	331	3	US-09-997-349-209	Sequence 209, App
28	260	12.2	331	3	US-09-997-653-209	Sequence 209, App
29	260	12.2	331	3	US-09-989-293A-209	Sequence 209, App
30	258.5	12.1	325	1	US-09-055-097-5	Sequence 5, Appli
31	258.5	12.1	325	2	US-09-373-902-5	Sequence 5, Appli
32	166	7.8	161	2	US-09-270-767-32073	Sequence 32073, A
33	166	7.8	161	2	US-09-270-767-47290	Sequence 47290, A
34	121.5	5.7	472	2	US-09-270-767-45443	Sequence 45443, A
35	116.5	5.5	413	2	US-10-104-047-2399	Sequence 2399, Ap
36	113.5	5.3	4472	1	US-08-804-227C-2	Sequence 2, Appli
37	112.5	5.3	872	1	US-08-491-357-3	Sequence 3, Appli
38	112.5	5.3	872	2	US-08-968-633-3	Sequence 3, Appli
39	112.5	5.3	872	2	US-09-196-466-3	Sequence 3, Appli
40	112.5	5.3	872	2	US-09-669-459A-3	Sequence 3, Appli
41	112.5	5.3	872	5	PCT-US96-10823-3	Sequence 3, Appli
42	112.5	5.3	3724	1	US-08-804-227C-10	Sequence 10, Appl
43	112.5	5.3	3724	1	US-08-804-198-4	Sequence 4, Appli
44	111.5	5.2	1053	2	US-09-902-540-12126	Sequence 12126, A
45	110.5	5.2	636	2	US-09-252-991A-21770	Sequence 21770, A

ALIGNMENTS

RESULT 1
US-09-459-133-2
; Sequence 2, Application US/09459133
; Patent No. 6416988
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
; FILE REFERENCE: 98-77
; CURRENT APPLICATION NUMBER: US/09/459.133
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/111,697
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (137)...(137)
; OTHER INFORMATION: Xaa is Gly or Ser
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(397)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-459-133-2

Query Match		99.8%	Score 2131;	DB 2;	Length 397;
Best Local Similarity		99.7%	Pred. No. 1.4e-192;		
Matches 396;		Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
Qy	1	MRCPKCLLSALLTLGLKVIWTSERLSKAYPSRGTTPSPPTPANPPTLPANLST	60		
Db	1	MRCPKCLLSALLTLGLKVIWTSERLSKAYPSRGTTPSPPTPANPPTLPANLST	60		
Qy	61	RLGOTIPLPAYWNOQWRGLSGSLPGSTGTGGCOAGAAAATIPDPASYPKDLRRLL	120		
Db	61	RLGOTIPLPAYWNOQWRGLSGSLPGSTGTGGCOAGAAAATIPDPASYPKDLRRLL	120		
Qy	121	SAACRSFQMLPGGGGVSSCSDTDPYLLLVKSEPRFAERQAVRETWGSFAPGIRL	180		
Db	121	SAACRSFQMLPGGGGVSSCSDTDPYLLLVKSEPRFAERQAVRETWGSFAPGIRL	180		
Qy	181	LFLGLSPVGEAGPDLDSLVAWESRRYSDLLWDFDVPFNOTLKDLLLLLAWLGRHCPVTS	240		
Db	181	LFLGLSPVGEAGPDLDSLVAWESRRYSDLLWDFDVPFNOTLKDLLLLLAWLGRHCPVTS	240		

Db 181 LFLGSPVGEAGDPLSLVAVESRRYSDDLWDLFDPVFNQTLKDLLLAWLGRHCPTVS 240
QY 241 FVLRAQDDAFVHTPALLAHLRALPASARSYLGEVFTQAMPLRPGGPFYVPESFFEGG 300
Db 241 FVLRAQDDAFVHTPALLAHLRALPASARSYLGEVFTQAMPLRPGGPFYVPESFFEGG 300
QY 301 YPAYASGGGVYTAGRLAPKLLRAARVAPFPEDVYTGICIRALGLVPOAHGFLTAWPA 360
Db 301 YPAYASGGGVYTAGRLAPKLLRAARVAPFPEDVYTGICIRALGLVPOAHGFLTAWPA 360
QY 361 DRTADHCAFRNLLVRLPLGPOASIRLWKLODPRLOC 397
Db 361 DRTADHCAFRNLLVRLPLGPOASIRLWKLODPRLOC 397

RESULT 2

US-09-459-133-13
; Sequence 13, Application US/09459133
; Patent No. 6416988
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
; FILE REFERENCE: 98-77
; CURRENT APPLICATION NUMBER: US/09/459.133
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/111,697
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-459-133-13

Query Match 74.7%; Score 1595; DB 2; Length 389;
Best Local Similarity 76.1%; Pred. No. 5,2e-142;
Matches 302; Conservative 22; Mismatches 65; Indels 8; Gaps 2;

QY 1 MRCPCILLCISALLTLGLKVYIEWTSESLKXAPSPRGTPSPPTANDEPTLPANLST 60
Db 1 MRCRKQOLCSALLTLGLKVYIEWTSESLKKA--EPRGALSPPTPNNAEPTLPNLSA 58
QY 61 RLQOTIPLPAYWQOQWRLGSLPSGSDSTETGCGQAWGAAATEIPDFASYPKDLRRFL 120
Db 59 RLQOTGLSSAYWQOQWRLGSLPSGSDSTETGCGQAWGAAATEIPDFASYPKDLRRFL 112
QY 121 SAACRSFPQWLPGGGSGVSSCSDTDVYLLAVKSEPGFAERQAVRETGSPAPGIRL 180
Db 113 SAACRSFPQWLPAGEGSPVASCSDKDVYLLAVKSEPGHFAARQAVRETGSPVAGTRL 172
QY 181 LFLGSPVGEAGDPLSLVAVESRRYSDDLWDLFDPVFNQTLKDLLLAWLGRHCPTVS 240
Db 173 LFLGSPVGEAGDPLSLVAVESRRYSDDLWDLFDPVFNQTLKDLLLAWLGRHCPTVS 232
QY 241 FVLRAQDDAFVHTPALLAHLRALPASARSYLGEVFTQAMPLRPGGPFYVPESFFEGG 300
Db 233 FVLQVQDDAFVHTPALLAHLRALPASARSYLGEVFTQAMPLRPGGPFYVPESFFEGG 292
QY 301 YPAYASGGGVYTAGRLAPKLLRAARVAPFPEDVYTGICIRALGLVPOAHGFLTAWPA 360
Db 293 YPAYASGGGVYTAGRLAPKLLRAARVAPFPEDVYTGICIRALGLVPOAHGFLTAWPA 352
QY 361 DRTADHCAFRNLLVRLPLGPOASIRLWKLODPRLOC 397
Db 353 DRTADHCAFRNLLVRLPLGPOASIRLWKLODPRLOC 389

RESULT 3

US-10-019-735-1

; Sequence 1, Application US/10019735
; Patent No. 7005279
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: No. 7005279e1 Polypeptides
; FILE REFERENCE: 11216W01
; CURRENT APPLICATION NUMBER: US/10/019,735
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: JP 99/183437
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: JP 2000/74757
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-019-735-1

Query Match 26.1%; Score 558; DB 3; Length 397;
Best Local Similarity 34.5%; Pred. No. 3.9e-44;
Matches 121; Conservative 69; Mismatches 131; Indels 30; Gaps 8;

QY 69 PFAYWQOQWRLG-----SLPSGSDSTETGG-----COAWGAAATEIPDFASYP 112
Db 55 PFAYWQOQWRLG-----SLPSGSDSTETGG-----COAWGAAATEIPDFASYP 113
QY 113 KDLRRFLLSNACRSFPQWLPGGGSGVSSCSDTDVYLLAVKSEPGFAERQAVRETGW 172
Db 114 DRFKDFLLYLRCHNYSLLI-----DQPKCAKK--PFLLLAIAKSLTPHFARRQAIRSWG 166
QY 173 SPAGP---IRLLPLLG-SPVGEAGDPLSLVAVESRRYSDDLWDLFDPVFNQTLKDLL 227
Db 167 QESNAGNQTVRVFLGQTPEDNHPDLSMDLKFSEKHQDILWNYRDTFFNLSLKEVL 226
QY 228 LLAWLGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPASARSYLGEVFTQAMPLRKP 287
Db 227 FLRWSTSCPDTEFVKGDDDFVNTTHILNYLSLSKTKAKOLFIDGDIVHAGPHRDKK 286
QY 288 GPYVPESEFEGGYPAYASGGGVYAGRLAPKLLRAARVAPFPEDVYTGICIRALGLV 347
Db 287 LKYIPEVYVYSGLYPPYAGGGGFLYSGHIALRLYHITDQVHLYPIDDVYTGICIRALGLV 346
QY 348 POAHGFLTAWPADRTADH-CAFRNLLVRLPLGPOASIRLWKLODPRLOC 397
Db 347 PEKHGFRFTDIEEKNNICSYDMLVHVRKQDEMIDWISQSAHLKC 397

RESULT 4

US-10-019-735-4
; Sequence 4, Application US/10019735
; Patent No. 7005279
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: No. 7005279e1 Polypeptides
; FILE REFERENCE: 11216W01
; CURRENT APPLICATION NUMBER: US/10/019,735
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: JP 99/183437
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: JP 2000/74757
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-019-735-4

Query Match 22.5%; Score 481; DB 3; Length 378;
Best Local Similarity 33.1%; Pred. No. 6.7e-37;

GenCore version 5.1.9
 Copyright (c) 1993 - 2006 Bioceleration Ltd.
 OM protein - protein search, using sw model
 Run on: September 21, 2006, 14:39:05 ; Search time 34.687 Seconds
 (without alignments)
 938.721 Million cell updates/sec

Title: US-10-539-834-16
 Perfect score: 1999
 Sequence: 1 TSESLSKAYSPRGTPPSP.....LGPQASIRLWQLQDPRLOQC 372

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:*
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 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pap:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H COMB.pap:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS COMB.pap:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE COMB.pap:*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1995	99.8	397	2	US-09-459-133-2
2	1474	73.7	389	2	US-09-459-133-13
3	558	27.9	397	3	US-10-019-735-1
4	474.5	23.7	378	3	US-10-019-735-4
5	464.5	23.2	372	3	US-10-019-735-3
6	460.5	23.0	378	2	US-09-482-180A-2
7	459.5	23.0	372	3	US-10-019-735-2
8	375.5	19.0	378	2	US-10-104-047-2503
9	344.5	17.2	422	2	US-09-831-630-10
10	337	16.9	326	1	US-09-055-097-6
11	337	16.9	326	1	US-09-373-902-6
12	337	16.9	326	2	US-09-831-630-11
13	322.5	16.1	378	1	US-09-055-097-1
14	322.5	16.1	378	2	US-09-373-902-1
15	322.5	16.1	393	2	US-09-949-016-11567
16	320.5	16.0	378	2	US-09-831-630-13
17	314	15.7	310	2	US-09-831-630-9
18	260	13.0	331	2	US-09-831-630-12
19	260	13.0	331	2	US-09-991-181-209
20	260	13.0	331	2	US-09-990-444-209
21	260	13.0	331	2	US-09-997-333-209
22	260	13.0	331	2	US-09-992-598-209
23	260	13.0	331	2	US-09-989-735-209
24	260	13.0	331	3	US-09-989-726-209
25	260	13.0	331	3	US-09-997-514-209
26	260	13.0	331	3	US-09-989-728-209

27 260 13.0 331 3 US-09-997-349-209 Sequence 209, App
 28 260 13.0 331 3 US-09-997-653-209 Sequence 209, App
 29 260 13.0 331 3 US-09-989-293A-209 Sequence 209, App
 30 258.5 12.9 325 1 US-09-055-097-5 Sequence 5, Appli
 31 258.5 12.9 325 2 US-09-373-902-5 Sequence 5, Appli
 32 166 8.3 161 2 US-09-270-767-32073 Sequence 32073, A
 33 166 8.3 161 2 US-09-270-767-47290 Sequence 47290, A
 34 121.5 6.1 472 2 US-09-270-767-47290 Sequence 47290, A
 35 112.5 5.6 872 1 US-08-491-357-3 Sequence 3, Appli
 36 112.5 5.6 872 2 US-08-968-633-3 Sequence 3, Appli
 37 112.5 5.6 872 2 US-09-196-466-3 Sequence 3, Appli
 38 112.5 5.6 872 2 US-09-669-459A-3 Sequence 3, Appli
 39 112.5 5.6 872 5 PCT-US96-10823-3 Sequence 3, Appli
 40 112.5 5.6 3724 1 US-08-804-227C-10 Sequence 10, Appli
 41 112.5 5.6 3724 1 US-08-804-198-4 Sequence 4, Appli
 42 112 5.6 4472 1 US-08-804-227C-2 Sequence 2, Appli
 43 111.5 5.6 1053 2 US-09-902-540-12126 Sequence 12126, A
 44 110.5 5.5 636 2 US-09-252-991A-21770 Sequence 21770, A
 45 109 5.5 794 2 US-09-252-991A-28569 Sequence 28569, A

ALIGNMENTS

RESULT 1
 US-09-459-133-2
 ; Sequence 2, Application US/09459133
 ; Patent No. 6416988
 ; GENERAL INFORMATION:
 ; APPLICANT: Conklin, Darrell C.
 ; APPLICANT: Yamamoto, Gayle
 ; APPLICANT: Jaepers, Stephen R.
 ; APPLICANT: Gao, Zeren
 ; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
 ; FILE REFERENCE: 98-77
 ; CURRENT APPLICATION NUMBER: US/09/459,133
 ; CURRENT FILING DATE: 1999-12-10
 ; PRIOR APPLICATION NUMBER: 60/111,697
 ; PRIOR FILING DATE: 1998-12-10
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 397
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: VARIANT
 ; LOCATION: (137)...(137)
 ; OTHER INFORMATION: Xaa is Gly or Ser
 ; NAME/KEY: VARIANT
 ; LOCATION: (1)...(397)
 ; OTHER INFORMATION: Xaa = Any Amino Acid
 US-09-459-133-2

Query Match 99.8%; Score 1995; DB 2; Length 397;
 Best Local Similarity 99.7%; Pred. No. 9.9e-183;
 Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TSESLSKAYSPRGTPPSPANPEPTLPANLSTRLGQTPLPAYWQQOWRLGSLPS 60
 Db 26 TSESLSKAYSPRGTPPSPANPEPTLPANLSTRLGQTPLPAYWQQOWRLGSLPS 85
 Qy 61 GDSLETGCGQAWGAAATEIPDFASYPKDLRRFLLSAACRSFPQWLPGGGSGVSSCSDT 120
 Db 86 GDSLETGCGQAWGAAATEIPDFASYPKDLRRFLLSAACRSFPQWLPGGGSGVSSCSDT 145
 Qy 121 DVPYLLIAVKSEPGRFAERQAVRETWGSAPGIRLLFLGSPVGEAGPDLSLVAWESRR 180
 Db 146 DVPYLLIAVKSEPGRFAERQAVRETWGSAPGIRLLFLGSPVGEAGPDLSLVAWESRR 205
 Qy 181 YSDILLWDFVDPNOTKDLLLAWLGRHCPVSVFLRAODDAFVHTPALLAHLRALPP 240

Db 206 YSDLLWDLVDFVFNQTLKDLLLAWLGRHCHPTSVFLRAQDDAFVHTPALLAHLRALPP 265
QY 241 ASARSLYLGEVFTQAMPLKPGPPVPSRPPGGVYAYASGGVVIAGRLAPWLLRAAA 300
Db 266 ASARSLYLGEVFTQAMPLKPGPPVPSRPPGGVYAYASGGVVIAGRLAPWLLRAAA 325
QY 301 RVAPPPFDVYTGICIRALGLVPOAHGFLTAWPADRTADHCAFRNLLVRLPLGPOASIR 360
Db 326 RVAPPPFDVYTGICIRALGLVPOAHGFLTAWPADRTADHCAFRNLLVRLPLGPOASIR 385
QY 361 LWKQLQDRLOC 372
Db 386 LWKQLQDRLOC 397

RESULT 2

US-09-459-133-13
; Sequence 13, Application US/09459133
; Patent No. 6416988

GENERAL INFORMATION:

; APPLICANT: Conklin, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
; FILE REFERENCE: 98-77
; CURRENT APPLICATION NUMBER: US/09/459,133
; CURRENT FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/111,697
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 13

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-459-133-13

Query Match 73.7%; Score 1474; DB 2; Length 389;
Best Local Similarity 75.0%; Pred. No. 8.5e-133;
Matches 279; Conservative 22; Mismatches 63; Indels 8; Gaps 2;

QY 1 TSERSLKAYPSRGRTPPTANPEPTLPANLSTRLGOTIPLPFAYWQQQWRGLSLPS 60
Db 26 TSERSLKKA--EPGRALPSPTPNABPTLPNLNLSRLGOTGPLSSAYWQQQRLGLVPS 83
QY 61 GDSLETGGCOAWGAAATEIPDASYPKDLRLLSAACRSFPQWLPGGGGVSSCSDT 120
Db 84 TD-----CQTGTVAASEILFILYQELRRFLLSAACRSFPLWLPAGEGSPVASCDK 137
QY 121 DVPYLLAVKSBPFAERQAVRETGWSPAPGIRLLFLGSPVGEAGPDLDSIWAVERR 180
Db 138 DVPYLLAVKSBPFAERQAVRETGWSPVAGTRLLFLGSPVGEAGPDLDSIWAVERR 197
QY 181 YSDLLWDLVDFVFNQTLKDLLLAWLGRHCHPTSVFLRAQDDAFVHTPALLAHLRALPP 240
Db 198 YGDLWDLVDFVFNQTLKDLLLAWLGRHCHPTSVFLRAQDDAFVHTPALLAHLRALPP 257
QY 241 ASARSLYLGEVFTQAMPLKPGPPVPSRPPGGVYAYASGGVVIAGRLAPWLLRAAA 300
Db 258 TWARSYLGEIETQAKPLKPGPPVPSRPPGGVYAYASGGVVIAGRLAPWLLRAAA 317
QY 301 RVAPPPFDVYTGICIRALGLVPOAHGFLTAWPADRTADHCAFRNLLVRLPLGPOASIR 360
Db 318 RVAPPPFDVYTGICIRALGLVPOAHGFLTAWPADRTADHCAFRNLLVRLPLGPOASIR 377
QY 361 LWKQLQDRLOC 372
Db 378 LWRHLWVPELOC 389

RESULT 3

US-10-019-735-1

; Sequence 1, Application US/10019735
; Patent No. 7005279
; GENERAL INFORMATION:
; APPLICANT: KYOWA HAKKO KOGYO CO., LTD
; TITLE OF INVENTION: No. 7005279e1 Polypeptides

; FILE REFERENCE: 11216W01
; CURRENT APPLICATION NUMBER: US/10/019,735
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: JP 99/183437
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: JP 2000/74757
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

; LENGTH: 397

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-019-735-1

Query Match 27.9%; Score 558; DB 3; Length 397;
Best Local Similarity 34.5%; Pred. No. 5.7e-45;
Matches 121; Conservative 69; Mismatches 131; Indels 30; Gaps 8;

QY 44 PPAVWQQQWRGLG-----SLPSGDSSTETGG-----COAGAAATEIPDFASYP 87
Db 55 PPAVWQQQWRGLG-----SLPSGDSSTETGG-----COAGAAATEIPDFASYP 113
QY 88 KDLRRELLAAACRSFPQWLPGGGGVSSCSDTDPVYLLAVKSEPCFAERQAVRETGW 147
Db 114 DRFKDFLLVRCNYSLLI-----DQDCAKK--PFLLAIKSLTPTFARRQAIRESWG 166
QY 148 SPAG-----IRLDFLLG-SPVGEAGPDLDSIWAVERRSDLLWDLVDFVFNQTLKDLL 202
Db 167 QESNAGNQTWVRFVFLGQTPEDNHPDLSDMLKFESEKQDILMNYRTDFNLSLKEVL 226
QY 203 LLAWLGRHCHPTSVFLRAQDDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLKPG 262
Db 227 FURWSTSCPDTEFVFKGDDVFNTHILNLSLSKTKAKDLFTGDVHNAGPHRDKK 286
QY 263 GPVYVPSFPEGGYPAYASGGVVIAGRLAPWLLRAAARVAPFPPEDVYTGICIRALGLV 322
Db 287 LKYYIPEVYVSLYPPYAGGGGFFVSGHLALRLYHTDOVHLYPDDVYTGICIRALGLV 346
QY 323 QPAHGFLLTAWPADTADH-CAFRNLLVRLPLGPOASIRLWKLQDRLOC 372
Db 347 PEKHGFRFTDEEKNKNICSYVDLMVHRSKPKQEMIDINWQLOSAHLKC 397

RESULT 4

US-10-019-735-4

; Sequence 4, Application US/10019735

; Patent No. 7005279

; GENERAL INFORMATION:

; APPLICANT: KYOWA HAKKO KOGYO CO., LTD

; TITLE OF INVENTION: No. 7005279e1 Polypeptides

; FILE REFERENCE: 11216W01

; CURRENT APPLICATION NUMBER: US/10/019,735

; CURRENT FILING DATE: 2001-12-28

; PRIOR APPLICATION NUMBER: JP 99/183437

; PRIOR FILING DATE: 1999-06-29

; PRIOR APPLICATION NUMBER: JP 2000/74757

; PRIOR FILING DATE: 2000-03-16

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 378

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-019-735-4

Query Match 23.7%; Score 474.5; DB 3; Length 378;
Best Local Similarity 39.3%; Pred. No. 5.4e-37;

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: September 21, 2006, 14:39:05 ; Search time 26.295 Seconds
(without alignments)
938.721 Million cell updates/sec

Title: US-10-539-834-17

Perfect score: 1508

Sequence: 1 RFLLSACRSFPQWLPFGG.....LGPOASIRLWKQLQDPRLQC 282

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /EMC/Celerra_SIDS3/ptodata/2/taa/7_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1504	99.7	397	2	US-09-459-133-2
2	1206	80.0	389	2	US-09-459-133-13
3	526.5	34.9	397	3	US-10-019-735-1
4	469.5	31.1	378	3	US-10-019-735-4
5	455.5	30.2	378	2	US-09-482-180A-2
6	427.5	28.3	372	3	US-10-019-735-3
7	422.5	28.0	372	3	US-10-019-735-2
8	379.5	25.2	378	2	US-10-104-047-2503
9	344.5	22.8	422	2	US-09-831-630-10
10	337	22.3	326	1	US-09-055-097-6
11	337	22.3	326	2	US-09-373-902-6
12	337	22.3	326	2	US-09-831-630-11
13	322	21.4	378	1	US-09-055-097-1
14	322	21.4	378	2	US-09-373-902-1
15	322	21.4	393	2	US-09-949-016-11567
16	320	21.2	378	2	US-09-831-630-13
17	314	20.8	310	2	US-09-831-630-9
18	260	17.2	331	2	US-09-831-630-12
19	260	17.2	331	2	US-09-991-181-209
20	260	17.2	331	2	US-09-590-444-209
21	260	17.2	331	2	US-09-997-333-209
22	260	17.2	331	2	US-09-992-598-209
23	260	17.2	331	2	US-09-989-735-209
24	260	17.2	331	3	US-09-989-726-209
25	260	17.2	331	3	US-09-997-514-209
26	260	17.2	331	3	US-09-989-728-209

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27 260 17.2 331 3 US-09-997-349-209 Sequence 209, App
28 260 17.2 331 3 US-09-997-533-209 Sequence 209, App
29 260 17.2 331 3 US-09-989-293A-209 Sequence 209, App
30 258.5 17.1 325 1 US-09-055-097-5 Sequence 5, Appli
31 258.5 17.1 325 2 US-09-373-902-5 Sequence 5, Appli
32 166 11.0 161 2 US-09-270-767-32073 Sequence 32073, A
33 166 11.0 161 2 US-09-270-767-47290 Sequence 47290, A
34 121.5 8.1 472 2 US-09-270-767-45443 Sequence 45443, A
35 105.5 7.0 113 2 US-09-270-767-46296 Sequence 46296, A
36 105.5 7.0 113 2 US-09-270-767-61866 Sequence 61866, A
37 101 6.7 174 2 US-09-270-767-60949 Sequence 60949, A
38 99 6.6 648 2 US-09-489-039A-10538 Sequence 10538, A
39 95 6.3 372 1 US-08-207-904-10 Sequence 10, Appl
40 93.5 6.2 542 2 US-09-252-991A-26256 Sequence 26256, A
41 93 6.2 274 2 US-09-252-991A-24164 Sequence 24164, A
42 92.5 6.1 1911 1 US-08-348-006B-5 Sequence 5, Appli
43 92.5 6.1 1911 1 US-08-800-825A-5 Sequence 5, Appli
44 92.5 6.1 1911 2 US-09-158-657-5 Sequence 5, Appli
45 92.5 6.1 1911 5 PCT-US94-10166-5 Sequence 5, Appli

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ALIGNMENTS

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RESULT 1
US-09-459-133-2
; Sequence 2, Application US/09459133
; Patent No. 6416988
; GENERAL INFORMATION:
; APPLICANT: Conklin, Darrell C.
; APPLICANT: Yamamoto, Gayle
; APPLICANT: Jaspers, Stephen R.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: BETA-1,3-GALACTOSYLTRANSFERASE HOMOLOGS
; FILE REFERENCE: 98-77
; CURRENT APPLICATION NUMBER: US/09/459,133
; PRIOR FILING DATE: 1999-12-10
; PRIOR FILING DATE: 1998-12-10
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (137)...(137)
; OTHER INFORMATION: Xaa is Gly or Ser
; FEATURES:
; NAME/KEY: VARIANT
; LOCATION: (1)...(397)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-459-133-2

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Query Match 99.7%; Score 1504; DB 2; Length 397;
Best Local Similarity 99.6%; Pred. No. 6.2e-149;
Matches 281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFLLSACRSFPQWLPFGGGSQVSSCSDTDPVYLLAVKSEPGRFABRQAVRTWGS 60
Db 116 RFLLSACRSFPQWLPFGGGSQVSSCSDTDPVYLLAVKSEPGRFABRQAVRTWGS 175
Qy 61 PGIRLLFILGSPVGEAGPDLDSLVAWESRRYSDDLMDFLDVPFNQTLKOLLALLGRH 120
Db 176 PGIRLLFILGSPVGEAGPDLDSLVAWESRRYSDDLMDFLDVPFNQTLKOLLALLGRH 235
Qy 121 CPTVSVFLRAODDAFVHTPALLAHLRALPPASASLYLGEVFTQAMPLKPGGPPYVPS 180
Db 236 CPTVSVFLRAODDAFVHTPALLAHLRALPPASASLYLGEVFTQAMPLKPGGPPYVPS 295
Qy 181 FFEQGYPAYASGGGVYTAGRLAPWLLRAAAARVAPPPEDVYTGLCIRALGVPOAHGFL 240

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Db 296 FFEQGYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLVPOAHGFL 355
QY 241 TAWPADRTADHCAFRNLLVRLPLGPOASIRLWKLODPRLOC 282
Db 356 TAWPADRTADHCAFRNLLVRLPLGPOASIRLWKLODPRLOC 397

RESULT 2
US-09-459-133-13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-019-735-1
Query Match 34.9%; Score 526.5; DB 3; Length 397;
Best Local Similarity 37.8%; Pred. No. 1.6e-46;
Matches 108; Conservative 58; Mismatches 107; Indels 13; Gaps 5;
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QY 63 ----IRLLFLLG-SPVGEAGPDLDSLVAVESRRYSDDLWDFLDPFNFOTLKDLLLAWL 117
Db 172 GNOTVVRVFLLGQTTPEDNHPDLSMLKFESEKHQDILWNYRDTFFNLSEVLFLRVV 231
QY 118 GRHCSTVSFVLRQADDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPQGPFFV 177
Db 232 STSCPDTEBFVKGDDDDVFVNTTHILNLYNLSLSTKAKDLFIGDVHNAAGPHRDKCLKYVI 291
QY 178 PRSPFEGGYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLVPOAHG 237
Db 292 FEVTSGLYPPYAGGGGFLYSGHLALRLYHTDQVHLYPIDDVYTGMCLOKLGLVPERKH 351
QY 238 GFLTAPADRTADH-CAFRNLLVRLPLGPOASIRLWKLODPRLOC 282
Db 352 GFRTDIEBKNNICSYDMLVHSRKPQEMIDWSQLOSAHLKC 397

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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-019-735-1
Query Match 31.1%; Score 469.5; DB 3; Length 378;
Best Local Similarity 39.4%; Pred. No. 1.4e-40;
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QY 58 ---SPAPGIRLLFLLGSPVGEAGPDLDSLVAVESRRYSDDLWDFLDPFNFOTLKDLLL 114
Db 145 GWAARGRLKLVFLLG-VAGSAPP--AQLLAYESREFDDILQWDFTEDEFNLTLLKELHLQ 201
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Db 202 RWWVAACPOAHFMKLGDDDDVFVHVPNVLEFLDGWDP--AQDLLVGDVIRQALPNNRTKVK 259
QY 175 FYPVESPFEG-GYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLV 233
Db 260 YFIPSPMYRATHYPPYAGGGYVMSRATVRRLQAIMEDAELFIDDDVFGVCLRLGLSP 319
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Db 296 FFEQGYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLVPOAHGFL 355
QY 241 TAWPADRTADHCAFRNLLVRLPLGPOASIRLWKLODPRLOC 282
Db 356 TAWPADRTADHCAFRNLLVRLPLGPOASIRLWKLODPRLOC 397

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; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-459-133-13
Query Match 80.0%; Score 1206; DB 2; Length 389;
Best Local Similarity 78.4%; Pred. No. 9.9e-118;
Matches 222; Conservative 18; Mismatches 42; Indels 0; Gaps 0;
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Db 108 RRFLLSAACRSFPQWLPGGGGSOVSSCSDTDVPYLLAVKSEPGFAERQAVRETWGSAP 167
QY 61 FGIRLLFLLGSPVGEAGPDLDSLVAVESRRYSDDLWDFLDPFNFOTLKDLLLAWLGRH 120
Db 168 AGTRLLFLLGSPVGEAGPDLDSLVAVESRRYSDDLWDFLDPFNFOTLKDLLLAWLGRH 227
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Db 228 CPDVNFVLQVODDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPQGPFFV 287
QY 181 FFEQGYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLVPOAHGFL 240
Db 288 FFEQGYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLVPOAHGFL 347
QY 241 TAWPADRTADHCAFRNLLVRLPLGPOASIRLWKLODPRLOC 282
Db 348 TAWPADRTADHCAFRNLLVRLPLGPOASIRLWKLODPRLOC 389

RESULT 3
US-10-019-735-1
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-019-735-1
Query Match 31.1%; Score 469.5; DB 3; Length 378;
Best Local Similarity 39.4%; Pred. No. 1.4e-40;
Matches 115; Conservative 38; Mismatches 114; Indels 25; Gaps 10;
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QY 58 ---SPAPGIRLLFLLGSPVGEAGPDLDSLVAVESRRYSDDLWDFLDPFNFOTLKDLLL 114
Db 145 GWAARGRLKLVFLLG-VAGSAPP--AQLLAYESREFDDILQWDFTEDEFNLTLLKELHLQ 201
QY 115 AYLGRHCHPTVSFVLRQADDAFVHTPALLAHLRALPPASARSLYLGEVFTQAMPLRKPQGP 174
Db 202 RWWVAACPOAHFMKLGDDDDVFVHVPNVLEFLDGWDP--AQDLLVGDVIRQALPNNRTKVK 259
QY 175 FYPVESPFEG-GYPAYAGGGYVIAGRLAPWLLRAAAARVAPFPFEDVYTGICIRALGLV 233
Db 260 YFIPSPMYRATHYPPYAGGGYVMSRATVRRLQAIMEDAELFIDDDVFGVCLRLGLSP 319
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; LENGTH: 397
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